

## **FIGURE 1**

GGACTAATCTGTGGGAGCAGTTATTCCAGTATCACCCAGGGTCAGCCACACCAGGACTGT  
GTTGAAGGGTGTCCCCCTAAATGTAATACCTCCTCATCTTCTTACACAGTG  
TCTGAGAACATTACATTATAGATAAGTAGTACATGGTGGATAACTCTACTTTAGGAGGA  
CTACTCTCTGACAGTCCTAGACTGGTCTTCTACACTAAAGACACCATGAAGGAGTATGTG  
CTCCTATTATTCCCTGGCTTGTGCTTGCAAACCCCTTTAGCCCTCACACATCGCACT  
GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATG  
ATGATGATGATGAGGACAACCTCTTTCCAACAAGAGAGCCAAGAAGCCATTTTCCA  
TTGATCTGTTCCAATGTGTCCATTGGATGTCAGTGCTATTCACTGAGTTGTACATTGCTC  
AGATTTAGGTTGACCTCAGTCCAAACCAACATTCCATTGATACTCGAATGCTTGATCTTC  
AAAACAATAAAATTAAGGAAATCAAAGAAAATGATTAAAGGACTCACTTCACTTATGGT  
CTGATCCTGAACAACAACAAGCTAACGAAGATTCAACCCAAAAGCCTTCTAACACAAAGAA  
GTTGCGAAGGCTGTATCTGCCCACAATCAACTAAAGTAAATACCACTTAATCTTCCAAAT  
CATTAGCAGAACTCAGAATTGATAAGAAAATGAGTCAACCCCTTGTATAAACACATTCAA  
GGAATGAATGCTTACACGTTGGAAATGAGTGCAAACCCCTTGTATAAACACATTCAA  
GCCAGGGGCATTGAAGGGGTGACGGTGTCCATATCAGAATTGAGAAGAAAATGACCT  
CAGTTCTAAAGGCTTACCAACTTATTGGAGCTTCACTTAGATTATAAAATTC  
ACAGTGGAACTTGAGGATTAAACGATAAAAGAAACTACAAAGGCTGGCCTAGGAAACAA  
CAAATCACAGATATCGAAAATGGGAGTCTGCTAACATACCACGTGTGAGAGAAATACATT  
TGGAAAACAATAAAACTAAAAAAATCCCTCAGGATTACCAAGAGTTGAAATACCTCCAGATA  
ATCTCCCTCATTCTAATTCAATTGCAAGAGTGGAGTAAATGACTCTGTCCAACAGTGCC  
AAAGATGAAGAAATCTTACAGTGCAATAAGTTATTCAACAAACCCGGTGAATACTGGG  
AAATGCAACCTGCAACATTGTTGTGTTGAGCAGAATGAGTGTCACTGGAAACTT  
GGAATGTAATAATTAGTAATTGGTAATGTCCTTAATATAAGATTCAAAATCCCTACATT  
TGGAAACTTGAACTCTATTAAATAATGGTAGTATTATATACAAGCAAATATCTATTCTCA  
AGTGGTAAGTCCACTGACTTATTGACAAGAAATTCAACGGAATTGCGTACAAATGAT  
GATACATAAGGGTTGAGAGAAACAAGCATCTATTGAGCTTCTTGTACAAATGAT  
CTTACATAAAATCTCATGCTGACCATTCTTCTTCATAACAAAAAGTAAGATATTGGTA  
TTAACACTTGTATCAAGCACATTAAAAGAACTGTACTGTAATGGAATGCTTGACT  
TAGCAAAATTGCTCTTCTTGCTGTTAGAAAAACAGAATTAACAAAGACAGTAATGT  
GAAGAGTGCATTACACTATTCTTATTCTTAGTAACCTGGTAGTACTGTAATATTTTAAT  
CATCTTAAAGTATGATTTGATATAATCTTATTGAAATTACCTTATCATGCTTAGAGCCGT  
CTTATGTTAAAACTAATTCTAAAATAAGCCTCAGTAAATGTTCTTGTACAAACTG  
TAAATGCTACTCATAGAGCTGGTTGGGCTATAGCATATGCTTTTTTTAATTATT  
ACCTGATTAAAATCTGTAAAACGTGTAGTGTTCATAAAATCTGTAACCTCGCATT  
AATGATCCGCTATTATAAGCTTTAATAGCATGAAAATTGTTAGGCTATATAACATTGCCAC  
TTCAACTCTAAGGAATATTTGAGATATCCCTTGGAAAGACCTGCTTGGAAAGAGCCTGGA  
CACTAACAAATTCTACACCAAATTGCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAA  
CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAAACAGACAGAAACCGAAAGCTCTA  
TATAAATGCTCAGAGTTCTTATGTATTCTTATTGGCATTCAACATATGTAACATCAGAAA  
ACAGGGAAATTTCATTAAAATATTGGTTGAAAT

## **FIGURE 2**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392
<subunit 1 of 1, 379 aa, 1 stop
<MW: 43302, pI: 7.30, NX(S/T): 1
MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDEDSLFPTRPR
SHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL
TSLYGLILNNNKLTKIHPKAFLTTKLRRLYLSHNQLSEIPLNLPKSLAELRIHENVKKIQ
KDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD
YNKISTVELEDFKRYKELQRLGLGNNKITDIENGLANIPRVREIHLENNKLKKIPSGLPEL
KYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV
QLGNFGM
```

PROTEIN "6592"

**Signal sequence.**

amino acids 1-15

**N-glycosylation site.**

amino acids 281-285

**N-myristoylation sites.**

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

**Leucine zipper pattern.**

amino acids 154-176

## **FIGURE 3**

## **FIGURE 4**

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSLPAPPAPLLLLGLLLLGSRPARGAGPEPPVLPIRSEKEPLPVRAAGCTFGGKVYALDE  
TWHPDLGQPGVVMRCVLCACEAPQWGRRTGPGRVSKNIKPECPTPACGQPRQLPGHCCQT  
CPQERSSSERQPSGLSFEYPRDPEHRSYSRGEPGAERARGDGHTDFVALLTGPRSQAVER  
ARVSLLRSSLRFSISYRRLDRPTRIRFSDNSGVLFEHPAAPTQDGLVCGVWRAPRLSLRL  
LRAEQLHVALVTLTHPSGEVGPLIRHALAAETFSAILTLEGPPQQGVGGITLLTLSDTED  
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQQLLRELQANVSAQE PGFAEVLPNLTVQEMD  
WLVLGELQMALEWAGRPGGLRISGHIAARKSCDVLQSVLCGADALIPVQTGAAGSASLTLLGN  
GSLIYQVQVVGTSSEVVAMTLETKPQRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAHML  
LQNELFLNVGTTKDFPDGELRGHVAALPYCGHSARHDTPVPLAGALVLPPVKSQAAGHAWLS  
LDTHCHLHYEVLLAGLGGSEQGTVAHLLGPPGTPGPRLLKGFYGSEAQGVVKDLEPELLR  
HLAKGMASLMITTGSPRGELRGQVHIANQCEVGLRLEAAGAEGVRALGAPDTASAAPPVV  
PGLPALAPAKPGGPGPRDPNTCFEGQQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVCP  
PPSCPHVQAPDQCCPVCPEKQDVRLPGLPRS RD PGE CYFDGDRSWRAAGTRWHPVVPPF  
GLIKCAVCTCKGGTGEVHCEKVQCPRLACAQPVRVNPTDCCKQCPVSGAHPQLGDPMQADG  
PRGCRFAGQWFPEQSWSHPSVPPFGEMSCITCRCGAGVPHCERDDCSLPLSCSGKESRCCS  
RCTAHRRRPETRTDPELEKEAEGS

**Signal sequence.**

amino acids 1-23

**N-glycosylation sites.**

amino acids 217-221, 351-355, 365-369, 434-438

**Tyrosine kinase phosphorylation sites.**

amino acids 145-153, 778-786

**N-myristoylation sites.**

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,  
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,  
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,  
905-911

**Amidation site.**

amino acids 87-91

**Cell attachment sequence.**

amino acids 165-168

**Leucine zipper pattern.**

amino acids 315-337

TIGESE00-6511660

## **FIGURE 5**

GGCGGGAGCAGCCCTAGCCGCCACCGTCGCTCTCGCAGCTCTCGTGCCTGCCACTGCCACCGCCGCCGTCACTGCG  
TCCTGGCTCCGGCTCCCGGCCCTCCCGGCCGGCATGCAGCCCCGCCGCCAGGCGCCGGTGCAGCTGC  
TGCCCGCGCTGGCCCTGCTGCTGCTGCTGGAGCGGGGCCCGAGGCAGCTCCCTGGCAACCCGGTGCCCG  
CCCGGCCCTTGTCTGCGCCCGGGCGTGCAGCCCTGCCGAAGCCCTGCCGAATGGGGTGTGCAACCTCGGCCCTG  
AGCCGGACCGCAGCACCCGGCCCCGCCGGAGGCAGCTACAGCTGCACCTGCCCGCCGGATCTCCGGCG  
CCAAC TGCCAGCTTGTGAGATCCTTGCCAGCAACCCCTGTCACCATGGCAACTGCAGCAGCAGCAGCA  
GCAGCAGCGATGGCTACCTCTGCAATTGCAATGAAGGCTATGAAGGTCAGACTGTGAACAGGCACTTCCCAGTC  
TCCCAGCCACTGGCTGGACCGAATCCATGGCACCCGACAGCTTCAGCCCTGCTACTCAGGAGCCTGACA  
AAATCCTGCCCTGCTCTCAGGCAACGGTACACTGCCCTACCTGGCAGCCGAAAACAGGGCAGAAAGTTGAGAAA  
TGAAATGGGATCAAGTGGAGGTGATCCAGATATTGCGCTGTGGAATGCCAGTTCTAACAGCTCTGCCGGTGGCC  
GCCTGGTATCCTTGAAAGTGCACAGAACACCTCAGTCAAGATTGGCAAGATGCCACTGCCACTGATTTCG  
TCTGGAAGGTACCGGCCACAGGATTCAAACAGTGCCTCCCTCATAGATGGACGAAGTGTGACCCCCCTTCAGGCTT  
CAGGGGGACTGGCTCTGGAGGAGATGCTGCCCTGGGAATAATCATTATTGGTTTGTGAATGATTCTG  
TGACTAAGTCTATTGCGCTTAACCTCTGGTGTGAAGGTACGCACCTGTGTGCCGGGGAGAGTCACG  
CAAATGACTTGGAGTGGTCAAGGAAAAGGAAATGCACACAGAAGCCGTAGAGGCAACTTTCTGTACCTGTG  
AGGAGCAGTACGTGGGTACTTCTGTGAAGAATACAGATGCTTGCAGAGGAAACCTTGCACAAACACGCGAGCT  
GTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTCACCTGTGTTGCCCTCTGGTTACTGGAGAGCTTT  
GCCAGTCAAAGATTGATTACTGCATCCTAGACCCATGCAGAAATGGAGCAACATGCATTTCAGTCTCAGTGGAT  
TCACCTGCCAGTGTCCAGAAGGAACTTCGGATCTGTTGTGAAGAAAAGGTGGACCCCTGCCCTCGTCTCCGT  
GCCAGAACACGGCACCTGCTATGTGGACGGGTACACTTACCTGCAACTGCAGCCGGGCTTCACAGGGCGA  
CCTGTGCCAGCTATTGACTTCTGTGCCCTCAGCCCTGTGCTCATGGCACGTGCCAGCGTGGCACAGCT  
ACAAATGCCCTGTGATCCAGGTTACCATGGCTCTACTGTGAGGAGGAATATAATGAGTGCCTCTCGCTCCAT  
GCCTGAATGCAGCCACCTGCAGGGACCTCGTAATGGCTATGAGTGTGTTGCCAGAATACAAAGGAACAC  
ACTGTGAATTGTACAAGGATCCCTGCGCTAACGTCAAGTCTGACGGAGCCACCTGTGACAGCGACGCCGTGA  
ATGGCACGTGCATCTGTGACCCGGTTACAGGTGAAGAGTGCACATTGACATAAATGAATGTGACAGTAACC  
CCTGCCACCATGGTGGAGCTGCCCTGGACCAGCCAATGGTTATAACTGCCACTGCCCATGGTGGGGAG  
CAAAC TGTGAGATCCACCTCCAATGGAAGTCCGGGACATGGGGAGAGCCTACCAACATGCCACGGCACTCCC  
TCTACATCATCATTGGAGCCCTCTCGTGGCCTTCATCCTATGCTGATCATCCTGATCGTGGGGATTGCCGCA  
TCAGCCGATTGAATACCAGGGTTCTCCAGGCCAGCCTATGAGGAGTTACAAC TGCCGCAGCATGACAGCG  
AGTT CAGCAATGCCATTGCATCCATCGGCATGCCAGGTTGAAAGAAATCCGGCTGCAATGTATGATGTGA  
GCCCATGCCCTATGAAGATTACAGTCCGTGATGACAACCCCTGGTCACACTGATTAAGAAACTAAAGATTG**TAAT**  
CTTTTTGGATTATTTCAAAAAGATGAGATACTACACTCATTTAAATATTAAAGAAAATAAAAGCTTAA  
GAAATTAAATGCTAGCTCAAGAGTTTCAGTAGAATATTAAAGAACTAATTTCAGCTTGTGAGCTTGTG  
GAAAAAAATATTAAACAAATTGTGAAACCTATAGACGATTTTAATGTACCTTCAGCTCTAAACTGT  
GTGCTTCTACTAGTGTGCTTTCACTGTAGACACTATCACGAGACCCAGATTAATTCTGTGGTTTACA  
GAATAAGTCTAATCAAGGAGAAGTTCTGTTGACGTTGAGTGCCTCTGAGTAGAGTTAGGAAAACCAC  
GTAACGTAGCATATGATGTATAATAGAGTATACCCGTTACTTAAAAAGAAGTCTGAAATGTTGTTGTGAAA  
AGAAAATAGTTAAATTACTATTCCAACCGAATGAAATTAGCCTTGCCTTATTCTGTGATGGTAAGTAAC  
TTATTCTGCACTGTTGTTGAACTTTGTGAAACATTCTTGCAGTTGTTGTGATTTCTGTAACAGTCG  
TCGAACTAGGCCCTAAAAACATACGTAACGAAAAGGCCAGCGAGGCAAATTCTGATTGATTGAATCTATATT  
TTCTTAAAAAGTCAAGGGTTCTATATTGTGAGTAATTAAATTACATTGAGTTGTTGTGCTAAGAGGTAG  
TAAATGTAAGAGAGTACTGGTCTCTCAGTAGTGAGTATTCTCATAGTGCAAGCTTATTATCTCCAGGATGTT  
TTGTGGCTGTATTGATTGATATGTGCTTCTGATTCTGCTAATTCCAACCATTGAATAATGTGATC  
AAGTCA

## **FIGURE 6**

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQLLPALLLLLLGGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSR  
PEPDPQHPAPAGEPGYSCTCPAGISGANCQLVADPCASNPCHGNCSSSSSSDGYLCICN  
EGYEGPNCEQALPSLPATGWTEMAPRQLQPVPATQEPDKILPRSQATVTLPTWQPKTGQKV  
VEMKWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFQ  
QCSLIDGRSVTPLQASGLVLLEEMLALGNNHFIGFVNDSVTKSIVALRLTLVVKVSTCVPG  
ESHANDLECSKGKCTTPSEATFSCTCEEQYVGTFCCEYDACQRKPCQNNASCIDANEKQD  
GSNFTCVCLPGYTGELCQSKIDYCILDPCRNGATCISSLSGFTQCPEGYFGSACEEKVDPC  
ASSPCQNNNGTCYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCSRSGTSYKCLCDPG  
YHGLYCEEYNECLSAPCLNAATCRDLVNGYECVCLAELYKGTCHCELYKDPCANVSCLNGATC  
DSDGLNGTCICAPGFTGEEDIDINECDSNPCHGGSCLDQPNNGYNCHCPHGWVGANCEIHL  
QWKSGHMAESLTNMPRHSLYIIIGALCVAFILMLIILIVGICRISRIEYQGSSRPAYEEFYN  
CRSIDSEFSNAIASIRHARFGKKSRPAMYDVSPIAYEDYSPDDKPLVTLIKTKDL

**Signal sequence.**

amino acids 1-28

**Transmembrane domain.**

amino acids 641-660

**N-glycosylation sites.**

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,  
375-379, 442-446, 549-553, 564-568

**Glycosaminoglycan attachment site.**

amino acids 320-324

**Tyrosine kinase phosphorylation sites.**

amino acids 490-498, 674-682

**N-myristoylation sites.**

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,  
373-379, 449-455, 480-486, 562-568, 565-571

**Amidation site.**

amino acids 702-706

**Aspartic acid and asparagine hydroxylation site.**

amino acids 520-532, 596-608

**EGF-like domain cysteine pattern signatures.**

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,  
491-503, 529-541, 567-579, 605-617

PROTEIN: 653030

## **FIGURE 7**

CTCTGGAAGGTACGGCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA  
CCCCCCTTCAGGCTTCAGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTGGGGAAATA  
ATCACTTTATTGGTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTGCGCTTAAC  
CTGGTGGTGAAGGTACGCACCTGTGCCCCGGAGAGTCACGCAAATGACTGGAGTGTTC  
AGGAAAAGGAAAATGCACCAACGAAGCCGTACAGAGGCAACTTTCCCTGTACCTGTGAGGAGC  
AGTACGTGGTACTTCTGTGAAGAATACGATGCTGCCAGAGGAAACCTGCCAAACAAAC  
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGAGCAATTACCTGTGTTGCCTTCC  
TGGTTATACTGGAGAGCTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT  
GAGATAGGGGAG

## **FIGURE 8**

CTCTGGAAGGTACGGCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA  
CCCCCCTTCAGGCTTCAGGGGACTGGCCTCCTGGAGGAGATGCTCGCCTGGGAATA  
ATCACTTATTGGTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTGCGCTTAAC  
CTGGTGGTGAAGGTACGCACCTGTGTGCCGGGGAGAGTCACGCAAATGACTGGAGTGTTC  
AGGAAAAGGAAAATGCACACGAAGCCGTACAGAGGCAACTTTCTGTACCTGTGAGGAGC  
AGTACGTGGTACTTCCTGTGAAGAATACGATGCTGCCAGAGGAAACCTGCCAAACAAAC  
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGAGCAATTACCTGTGTTGCCTCC  
TGGTTATACTGGAGAGCTTGCCAACCGAACCTGAGATTGGAGCGAACGACCTACACCGAACT  
GAGATAGGGAG

## **FIGURE 9**

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GCTGAGTCTGCTGCTCCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG  
GCCCCCCCAGAGCCCTCACCAACGCTGGCGCCCCAGAGCCCACACCATGCCGGGCACCTAC  
GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGCCCT  
GATGCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCTGGCCTAAGGCAGGTTT  
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTCAGCTACGGCCAGACCAGCCTGGAC  
AGGCTTAGAGATGGCCTCGTGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA  
GGACCGGGATGCCCTGCGCCTCACCCGGAGCAGATTGACCTCATGCCGATGTGTGCCT  
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC  
TGCCTCATCGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATTTACGTACCTT  
CTACATGCTGGAGTGCGCTACCTGACGCTCACCCACACCTGCAACACACCCCTGGCAGAGA  
GCTCCGCTAAGGGCGTCCACTCCTTCTACAACAAACATCAGCGGGCTGACTGACTTTGGTGAG  
AAGGTGGTGGCAGAAATGAACCGCCTGGCATGATGGTAGACTTATCCATGTCTCAGATGC  
TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTCTCCACTCGGCTGCC  
GGGGTGTGTGCAACAGTGCTCGGAATGTTCTGATGACATCCTGCAGCTCTGAAGAAGAAC  
GGTGGCGTCGTGATGGTGTCTTGTCCATGGAGTAATAACAGTGCAACCCATCAGCCAATGT  
GTCCACTGTGGCAGATCACTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGA  
TTGGTGGAGATTATGATGGGCCGGCAAATTCCCTCAGGGGCTGGAAGACGTGTCCACATAC  
CCGGTCCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCC  
TCGTGGAAACCTGCTGCGGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGC  
AAAGCCCCCTGGAGGACAAGTTCCGGATGAGCAGCTGAGCAGTTCTGCCACTCCGACCTC  
TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACACTGAGATTCCATACA  
CTGGACAGCCAAGTTACCAAGCCAAGTGGTCAGTCTCAGAGTCCCTCCCCCAGATGGCC  
TCCTTGAGTTGTGGCCACCTTCCAGTCCTTATTCTGTGGCTTGATGACCCAGTTAGTCC  
TGCCAGATGTCACTGTAGCAAGCCACAGACACCCACAAAGTTCCCTGTTGTGCAGGCACA  
AATATTCTGAAATAATGTTGGACATAG

## **FIGURE 10**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595
<subunit 1 of 1, 433 aa, 1 stop
<MW: 47787, pI: 6.11, NX(S/T): 5
MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDSLHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVVMVSLSMGVIQCNPNSANVSTVADHFDHIKAVIGSKFIGIGGYDGAGKFPQGLE
DVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEEENKWQSPLEDKFPDEQLSSS
CHSDLRSRLQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLAVVATFPVLILWL
```

**N-glycosylation sites.**

amino acids 58-62, 123-127, 182-186, 273-277

**N-myristoylation sites.**

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

**Renal dipeptidase active site.**

amino acids 134-157

## **FIGURE 11**

AAAACCTATAAATATTCCGGATTATTCAACCGTCCCACCATCGGGCGCGGATCCGCGGCCG  
CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA  
CCCAGGGCCTGCAAGAGCAGGCACGGGCCTGATGCGGGACTTCCGCTCGTGGACGGCCAC  
AACGACCTGCCCTGGTCCTAAGGCAGGTTACCAGAAAGGGCTACAGGATGTTAACCTGCG  
CAATTCAGCTACGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGCGCCAGT  
TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACGGGATGCCCTGCGCCTCACCTGGAG  
CAGATTGACCTCATGCCGCATGTGTGCCCTATTCTGAGCTGGAGCTTGACCTCGGC  
TAAAGCTCTGAACGACACTCAGAAATTGCCCTGCCTCATCGGTGTAGAGGGTGGCACTCGC  
TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGAGTGCCTACCTGACGCTC  
ACCCACACCTGCAACACACCCCTGGCAGAGAGCTCCGCTAAGGGGTCCACTCCTTACAA  
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGCAGAAATGAACCGCTGGCA  
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTACAG  
GCACCTGTGATCTTCTCCACTCGGCTGCCGGGGTGTGCAACAGTGTCTGGAAATGTTCC  
TGATGACATCCTGCAGCTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTGCCATGG  
GAGTAATACAGTCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTCGACCAACATC  
AAGGCTGTCATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAATT  
CCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGCCTGATAGAGGAGTTGCTGAGTCGTG  
GCTGGAGTGGAGAACGGCTTCAGGGTGTCCCTCGTGGAAACCTGCTGCGGGCTTCAGACAA  
GTGGAAAAGGTACAGGAAGAAAACAATGGCAAAGGCCCTGGAGGACAAGTTCCGGATGA  
GCAGCTGAGCAGTTCCTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACAGAGTCTGACTT  
CAGGCCAGGAACACTCACTGAGATTCCCACACTGGACAGCCAAGTTACCAAGCCAAGTGGTCA  
GTCTCAGAGTCCTCCCCCACCCTGACAAAACACATGCCAACCGTGCCAGCACCTGA  
ACTCCTGGGGGGACCGTCAGTCTCCTCTTCCCCCAAAACCCAAGGACACC

## **FIGURE 12**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872
><subunit 1 of 1, 446 aa, 0 stop
><NX(S/T): 5
MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRRMCAASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTHTCNPWAESSAKGVHSFYNNISGL
TDFGEKVVVAEMNRLLGMMVDSLHVSDAARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEEWKQSPLEDKFPDEQLSSS
CHSDLRQLRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHPDKTHTCPPCPAPELLGGP
SVFLFPPPKPKDT
```

## **FIGURE 13**

CGCCCAGCGACGTGCGGGCGGCCTGGCCCCGCCCTCCCGCGCCCGGCCTGCGTCCCGGCC  
CTGCGCCACCGCCGCCGAGCGCAGCCCAGCGCGCCGCCGGCAGCGCCGCCATGCCC  
GCCGGCCGCCGGGGCCCCGCCAATCCGCGCGCGGCCGCCGTTGCTGCCCTGCT  
GCTGCTGCTCTGCGTCCTCGGGCGCCGAGCGGATCAGGAGCCCACACAGCTGTGATCA  
GTCCCCAGGATCCCACGCTTCTCATCGGCTCCTCCCTGCTGGCCACCTGCTCAGTGCACGGA  
GACCCACCAGGAGCCACCGCCGAGGGCCTCTACTGGACCTCAACGGCGCCGCCCTGCC  
TGAGCTCTCCCGTGTACTCAACGCCCTCACCTGGCTCTGCCCTGCCAACCTCAATGGGT  
CCAGGCAGCGGTGCGGGGACAACCTCGTGTGCCACGCCGTGACGGCAGCATTGGCTGGC  
TCCTGCCTCTATGTTGGCCTGCCCTCAGAGAAACCGTCAACATCAGCTGCTGGTCCAAGAA  
CATGAAGGACTTGACCTGCCGCTGGACGCCAGGGCCCACGGGGAGACCTTCCTCACACCA  
ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGCCAGGACAACACATGTGAGGAGTACCA  
ACAGTGGGCCCACTCCTGCCACATCCCCAAGGACCTGGCTCTTTACGCCCTATGAGAT  
CTGGGTGGAGGCCACCAACGCCCTGGCTCTGCCGCTCCGATGTACTCACGCTGGATATCC  
TGGATGTGGTGACCAACGGACCCCCCGCCGACGTGACGTGAGGCCGTCGGGGCCTGGAG  
GACCAGCTGAGCGTGCCTGGGTGCGCACCCGCCCTCAAGGATTCCCTTTCAAGCAA  
ATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGACGATGTGAGCA  
ACCAGACCTCCTGCCCTGGCCGGCTGAAACCCGGCACCGTGTACTCGTCAAGTGC  
TGCAACCCCTTGGCATCTATGGCTCCAAGAAAGCCGGATCTGGAGTGAGTGGAGCCACCC  
CACAGCCGCTCCACTCCCCGCACTGAGCGCCGGGCCGGCGGGCGTGCACCGC  
GGGGCGGAGAGCCGAGCTGGGCCGGTGCAGCGAGCTCAAGCAGTCCGGCTGGCT  
AAGAAGCACCGTACTGCTCCAACCTCAGCTCCGCCCTACGACCAGTGGCGAGCCTGGAT  
GCAGAAGTCGCACAAGACCCGCAACCAGGACGAGGGATCCTGCCCTGGCAGACGGGCA  
CGCGAGAGGTCTGCCAGATAAGCTGTAGGGCTCAGGCCACCCCTGCCACGTGGAGA  
CGCAGAGGCCGAACCAAACGGGCCACCTCTGTACCCCTACCCAGGGCACCTGAGGCCAC  
.CCTCAGCAGGAGCTGGGTGGCCCTGAGCTCCAACGCCATAACAGCTCTGACTCCACGT  
GAGGCCACCTTGGGTGCACCCAGTGGGTGTGTGTGAGGGTTGGTTGAGTTGC  
CTAGAACCCCTGCCAGGGCTGGGGTGAGAAGGGAGTCATTACTCCCCATTACCTAGGGCC  
CCTCCAAAAGAGTCCTTAAATAATGAGCTATTAGGTGCTGTGATTGTGAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAACAAAAAAA

## **FIGURE 14**

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pI: 9.42, NX(S/T): 6

MPAGRRGPAAQSARRPPPLPLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSV  
HGDPPGATAEGLYWTNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSIL  
AGSCLYVGLPPEKPVNISCKSNMKDLTCRWTGAHGETFLHTNYSLKYLWYGQDNTCEE  
YHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLIDLDVVTTDPPPDVHSRVGG  
LEDQLSVRWVSPPALKFQAKYQIRYRVEDSVDKVVDDVSNQTSCRLAGLKPGTVYFVQ  
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGACEPRGGEPSGPVRRELKQFLG  
WLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRRGRTARGPAR

**Signal sequence.**

amino acids 1-30

**Transmembrane domain.**

amino acids 44-61

**N-glycosylation sites.**

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 413-417

**N-myristylation sites.**

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,  
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

**Amidation site.**

amino acids 3-7, 79-83, 411-415

**Growth factor and cytokines receptors family signature 2.**

amino acids 325-331

## FIGURE 15

## **FIGURE 16**

```
</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436
<subunit 1 of 1, 300 aa, 1 stop
<MW: 32964, pI: 9.52, NX(S/T): 1
MKFLLDILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKGLGAKVHTFVVDCSNREDIYSSAKKVKAEGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ
```

**Signal sequence.**

amino acids 1-19

**Transmembrane domain.**

amino acids 170-187

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 30-34, 283-287

**N-myristoylation sites.**

amino acids 43-49, 72-78, 122-128, 210-216

TOP SECRET//SI//NOFORN

## **FIGURE 17**

GAAGTTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCGAGACTG  
GGGTGACGGCAGGGCAGGGGGCGCTGGCCGGGAGAAGCGCGGGGCTGGAGCACCAAA  
CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGAGCCGGAGGGGGACT  
GCGAGAGGACCCCGCGTCCGGCTCCGGTGCAGCGCTATGAGGCCACTCCTCGTCCTGC  
TGCTCCTGGGCCTGGCGGGCCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGC  
CCGGGGCACCCGGCCTTCCAGGCACGCCGGCCACCATTGGCAGGCCAGGGCTGCCGGCG  
CGATGGCCGCGACGCCCGACGCCCGCCAGGGAGAGAAAGGCAGGGCG  
GGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGCGAGGGAGAGGCCAGGGACCCGGGG  
CCCACCGGGCTGCCGGGAGTGCTCGGTGCCTCCCGATCCGCTTCAGGCCAAGCGCTC  
CGAGAGCCGGTGCCTCCCGTCTGACGCCACCTGCCCTCGACCGCGTGCTGGTAACG  
AGCAGGGACATTACGACGCCGTACCGCAAGTTCACCTGCCAGGTGCCTGGGTCTACTAC  
TTCGCCGTCCATGCCACCGTCTACCGGCCAGCCTGCAGTTGATCTGGTAAGAATGGCGA  
ATCCATTGCCCTTTCTTCCAGTTTCGGGGGTGGCCAAGCCAGCCTCGCTCTCGGGGG  
GGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGTGACTAC  
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTCTCCGGATTCTGGTGTACTCCGA  
CTGGCACAGCTCCCCAGTCTTGCTTAGTGCCACTGCCAAAGTGAGCTATGCTCTCACTCC  
TAGAAGGAGGGTGTGAGGCTGACAACCAGGTATCCAGGAGGGCTGGCCCCCTGGAATATT  
GTGAATGACTAGGGAGGTGGGTAGAGCACTCTCCGTCTGCTGGCAAGGAATGGAAC  
AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGCAGTGGCTGGATTCTGCCAAGACCA  
GAGGAGTGTGCTGTGCTGGCAAGTGTAAAGTCCCCAGTTGCTCTGGTCCAGGAGGCCACGGT  
GGGGTGCCTCTTCCTGGCCTCTGCTTCTGGATCCTCCCCACCCCTCCTGCTCCTGGG  
GCCGCCCTTCTAGAGATCACTCAATAAACCTAAGAACCTCATAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAA

## **FIGURE 18**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592

><subunit 1 of 1, 243 aa, 1 stop

><MW: 25298, pI: 6.44, NX(S/T): 0

MRPLLVLLLLGLAAGSPPPLDDNKIPSLCPGHPGLPGTPGHGSQGLPGRDGRDGRDGAPGAP  
GEKGEGRGPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLP  
FDRV LVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP  
KPASLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKT DSTFSGFLVYSDWHSSPVFA

**Signal sequence.**

amino acids 1-15

**N-myristoylation sites.**

amino acids 11-17, 68-74, 216-222

**Cell attachment sequence.**

amino acids 77-80

\* 6085984 6085985 6085986 6085987

## **FIGURE 19**

CTCTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG  
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCAACAGACCCAT  
GCTGCATCCAGAGACCTCCCCTGGCGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTG  
GCACCACCTGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC  
CTGAACAGGAAGGAGAGTTCCTGCTCCTCCCTGCACAACCGCCTGCGCAGCTGGTCCA  
GCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCAAGTGGCTCAAG  
CCAGGGCAGCCCTGTGGAATCCAACCCGAGCCTGGCATCCGGCTGTGGCGCACCTG  
CAAGTGGCTGGAACATGCAGCTGCTGCCCGGGCTTGGCTCCTTGTGAAGTGGTCAG  
CCTATGGTTGCAGAGGGCAGCGGTACAGCCACGCGGAGGAGTGCTCGCAACGCCA  
CCTGCACCCACTACACGCAGCTCGTGTGGCCACCTCAAGCCAGCTGGCTGTGGCGCAC  
CTGTGCTCTGCAGGCCAGACAGCGATAGAACGCTTGTCTGCCTACTCCCCGGAGGCAA  
CTGGAGGTCAACGGAAAGACAATCATCCCTATAAGAAGGGTGCCTGGTGTGCTGCA  
CAGCCAGTGTCTCAGGCTGCTCAAAGCCTGGACCATGCAGGGGGCTCTGTGAGGTCCCC  
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGTCTAACATCAGCACCTGCCACTG  
CCACTGTCCCCCTGGCTACAGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTG  
ACGGCCGGTCCGGGAGGAGGAGTGCTCGTGTGACATCGGCTACGGGGAGGCCAG  
TGTGCCACCAAGGTGCATTTCCCTCACACCTGTGACCTGAGGATCGACGGAGACTGCTT  
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCG  
GGGTGCTGGCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTGCCCTATCTGGCCGC  
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACCTCTGGATGGGCT  
CACCTACAAGACCGCCAAGGACTCCTCCGCTGGCCACAGGGAGCACAGGCCCTCACCA  
GTTTGCCCTTGGCAGCCTGACAACCACGGCTGGTGTGGCTGAGTGCTGCCATGGGTTT  
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCCTCAACTGGAACGACCAGCGCTGAAAAC  
CCGAAACCGTTACATCTGCCAGTTGCCAGGAGCACATCTCCGGTGGGCCAGGGCCT  
GAGGCCTGACCACATGGCTCCCTGCCCTGGGAGCACCAGGCTCTGCTTACCTGTCTGC  
CCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACTGCCATGTCCAAAGAGGTCTCAGA  
CCTTGACAATGCCAGAAGTTGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG  
AGTGTAGAAGAAGCTGGGCCCTCGCCTGCTTGTGATTGGGAAGATGGGCTTCAATTAGA  
TGGCGAAGGAGAGGACACCGCCAGTGGTCAAAAAGGCTGCTCTTCCACCTGGCCAGAC  
CCTGTGGGGCAGCGGAGCTCCCTGTGGCATGAACCCACGGGTATTAAATTATGAATCAG  
CTGAAAAAAAAAAAAA

## **FIGURE 20**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176  
<subunit 1 of 1, 455 aa, 1 stop  
<MW: 50478, pI: 8.44, NX(S/T): 2  
  
MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEAPMAGALNRKESFLLSLHNRLRSWV  
QPPAADMRRLDWSDSLAAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV  
SLWFAEGQRYSHAAGECARNATCTHYTQLWATSSQLGCGRHLCAGQTAIEAFVCAYSPGG  
NWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSQNHGRLNISTCH  
CHCPCPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFHTCDLRIDGDC  
FMVSSEADTYYRARMKCQRKGGLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIG  
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCK  
TRNRYICQFAQEHIWRWGPSS  
  
**Signal sequence.**  
amino acids 1-26  
  
**Transmembrane domain.**  
amino acids 110-124  
  
**N-glycosylation sites.**  
amino acids 144-148, 243-247  
  
**cAMP- and cGMP-dependent protein kinase phosphorylation site.**  
amino acids 45-49  
  
**N-myristoylation sites.**  
amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,  
288-294, 331-337, 398-404  
  
**Prokaryotic membrane lipoprotein lipid attachment site.**  
amino acids 204-215  
  
**EGF-like domain cysteine pattern signature.**  
amino acids 249-261, 280-292  
  
**C-type lectin domain signature.**  
amino acids 417-442

## **FIGURE 21**

CGGACGCGTGGGCTGGGCCTGCAAAGCGTGTCCGCCGGTCCCCGAGCGTCCCCGCGCCCTCGCCCGCCATGCTCCTGCTGCTGGGGCTGTGCCTGGGGCTGTCCCTGTGTGTGGGGTCGA  
GGAAGAGGCGCAGAGCTGGGCCACTCTCGGAGCAGGATGGACTCAGGGTCCCAGGCAAGTCAGACTGTTGAGGGCTGAAAACAAACCTTGATGACAGAATTCTCAGTGAAGTCTACC  
ATCATTTCCCGTTATGCCTTCACTACGGTTCCACTGCAGAATGCTGAACAGAGCTTCTGAAGAAGGACATTGAGTTCCAGATGCAGATTCCAGCTGCAGCTTCACTACCATG  
TTATTGGAGACAAGGTGTATCAGGGCAAATTACAGAGAGAGAAAAGAAGAGTGGTGATAGGGTAAAGAGAAAAGGAATAAAACACAGAAGAAAATGGAGAGAAGGGGACTGAAATATT  
AGCTTCTGCAGTGATTCCAGCAAGGACAAGGCCCTTTCTGAGTTATGAGGAGCTTCAGCAGGAGCACAGCATCAGCGTGCAGGCCAGCAGCTGTCCGG  
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCC  
GCTTCACAACAGCAGGCAGAGGGCAGTGGCGCGGGAAAGATGATTCTGGCCTCCCCCAT  
CTACTGTCACTAACCAAAATGAAACATTGCCAACATAATTAAACCTACTGTAGTACAA  
CAAGCCAGGATTGCCAGAATGGAATTGGAGACTTATCATTAGATATGACGTCAATAG  
AGAACAGAGCATTGGGACATCCAGGTTCTAAATGGCTATTGACTACTTGCTCCTAA  
AAGACCTTCCTCCTTACCCAAGAATGTGGTATTCTGCTGACAGCAGTGCTCTATGGTG  
GGAACCAAACCTCCGGCAGACCAAGGATGCCCTCTCACAAATTCTCATGACCTCCGACCCCA  
GGACCGTTCACTATTGGATTTCACCGGATCAAAGTATGGAAGGACCACTGATAT  
CAGTCACTCCAGACAGCATCAGGGATGGAAAGTGTACATTACCATATGTCACCCACTGGA  
GGCACAGACATCAACGGGCCCTGCAGAGGGCCATCAGGCTCCTCAACAAGTACGTGGCCCA  
CAGTGGCATTGGAGACCGGAGCGTGTCCCTCATCGTCTTGTACGGATGGGAAGGCCACGG  
TCGGGAGACGCACACCTCAAGATCCTCAACACACCCGAGAGGCCGCCAGGCCAGTC  
TGCATCTTCACCATTGGCATCGCAACGACGTGGACTTCAGGCTGCTGGAGAAACTGTCGCT  
GGAGAACTGTGGCCTCACACGGCGGTGCACGAGGGAGGAGCAGCAGGCTCGCAGCTCATCG  
GGTTCTACGATGAAATCAGGACCCGCTCCTCTGACATCCGATCGATTATCCCCCAGC  
TCAGTGGTGCAGGCCACCAAGACCCCTGTCCTCTGACATCCGATCGATTATCCCCCAGC  
TGCAGGAAAGCTGGTGACAGGAAGCTGGATCACCTGCACGTGGAGGTACCGCCAGCAACA  
GTAAGAAATTCATCATCCTGAAGACAGATGTGCCTGTGCGGCCCTCAGAAGGCAGGGAAAGAT  
GTCACAGGAAGCCCCAGGCCTGGAGGCATGGAGAGGGGACACCAACCACATCGACGTCT  
CTGGAGACTACCTCACCACAAAGGAGCTGCTGAGCTCCTGGCTGCAAAGTGCAGATGAACCGG  
AGAAGGAGCGGCTGCAGCAGGCCAGGCCCTGGCTGTGAGCTACCGCTTCTCACTCCC  
TTCACCTCCATGAAGCTGAGGGGCCGGTCCCACGCATGGATGGCCTGGAGGGGCCACGG  
CATGTCGGCTGCCATGGGACCCGAACCGGTGGTGAGAGCGTGCAGAGGAGCTGGCACGCAGC  
CAGGACCTTGCTCAAGAAGCCAAACTCCGTCAAAAAAAACAAAACAAAACAAAAAAAGA  
CATGGGAGAGATGGTGTGTTCTCCACCACTGGGATACGATGAGAAGATGGCCACCT  
GCAAGGCCAGGAAGACGCCCTCACAGACACCATGTCTGCTGGCACCTGATCTGGACCTC  
CCAGCCTCCAGAAGTGTGAGAAATAATGTGTTAAGCTAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 22**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192  
<subunit 1 of 1, 694 aa, 1 stop  
<MW: 77400, pI: 9.54, NX(S/T): 6  
  
MLLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLQLKTKPLMTEFSVKSTIIS  
RYAFTTVSCRMLNRASEDQDIEFQMGI PAAAFITNFTMLIGDKVYQGEITEREKSGDRVKE  
KRNKTEENGEKGTEIFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLS  
VDVNILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPSTVINQNETFANIIFKPTVVQQAR  
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFVLDSSASMVGTK  
LRQTKDALFTILHDLRPQDRFSIIGFSNRIKVWKDHLISVTPDSIRDGKVYIHMSPTGGTD  
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNNTREAARGQVCIF  
TIGIGNDVDFRLLEKLSLENGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV  
QATKTLFPNYFNGSEIIIAGKLVDRKLDHLHVEVTASNNSKKFIILKTDVPVRPQKAGKDVTG  
SPRPGGDGEGLTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS  
MKLRGPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKQNKTKRHGR  
DGVFPLHHLGIR

**Signal sequence.**

amino acids 1-14

**N-glycosylation sites.**

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

**Glycosaminoglycan attachment sites.**

amino acids 213-217, 391-395

**N-myristoylation sites.**

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

## **FIGURE 23**

CGGACGCGTGGGTGCCGACATGCGAGTGTAGTGCTGCCGAGCGGATCCAGTGTGCGGC  
GGCAGCGGCGGCCGGCGCTCCCGGGCTCCGGCTCTGCTGTTGCTCTTCTCCGCGCGG  
CACTGATCCCCACAGGTGATGGCAGAATCTGTTACGAAAGACGTGACAGTGATCGAGGGA  
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTCACTGAA  
TCCCAACAGGCAGACCATTATTCAGGGACTTCAGGCCTTGAAGGCACAGCAGGTTCACTG  
TGCTGAATTCTAGCAGTGAACCAAAGTATCATTGACAAACGTCTCAATTCTGATGAA  
GGAAGATACTTTGCCAGCTCTACCGATCCCCACAGGAAAGTTACACCACCATCACAGT  
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG  
AGATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCAGCAGCAGTATCAGGTGGTCAAA  
GGGAACACAGAGCTAAAGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC  
CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGTCCCAGTGATCTGCCAGGTGG  
AGCACCCCTGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT  
CAAGTGCACATTCACTGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGA  
GTTAACATGTGAAGCCATCGGAAGCCCCAGCCTGTGATGGTAACCTGGTGAGAGTCGATG  
ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCAACCTGTTCAATAAACCTAAACAAA  
ACAGATAATGGTACATACCGCTGTGAAGCTCAAACATAGTGGGAAAGCTCACTCGGATT  
TATGCTGTATGTATACGATCCCCCACAACATCCCTCCTCCCACAACAACCACCA  
CCACCACCACCACCACCATCCTTACCATCATCACAGATTCCCGAGCAGGTGAAGAAGGC  
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGGTGGTGG  
GCTGTGCTTGCTCATCATTCTGGGGCGCTATTGCCCCAGACATAAGGTACATACTCACTC  
ATGAAGCCAAGGGAGCCGATGACGCAGCAGCAGACACAGCTATAATCAATGCAGAAGGA  
GGACAGAACAACTCCGAAGAAAAGAAAGAGTACTTCATCTAGATCAGCCTTTGTTCAAT  
GAGGTGTCCAATGGCCCTATTAGATGATAAAGAGACAGTGATATTGG

## **FIGURE 24**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518
<subunit 1 of 1, 440 aa, 1 stop
<MW: 48240, pI: 4.93, NX(S/T): 7
MASVVLPSGSQCAAAAAAAPPGLRLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISC
QVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVISDEGRYFCQL
YTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTTELKG
KSEVEEWSDMYTVTSQMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMT
YPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYR
CEASNIVGKAHSYMLYVYDPPTTIPPPTTTTTTTTILTIITDSRAGEEGSIRAVDH
AVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEE
KKEYFI
```

**Signal sequence.**

amino acids 1-36

**Transmembrane domain.**

amino acids 372-393

**N-glycosylation sites.**

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,  
430-434

**Tyrosine kinase phosphorylation sites.**

amino acids 233-240, 319-328

**N-myristoylation sites.**

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,  
411-417, 427-433, 428-432

## **FIGURE 25**

GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCTCGGGCCGA  
CCGCCAGGAAAGACTGAGGCCGCGCCTGCCCGCCGGCTCCCTGCGCCGCCGCCCTC  
CCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGCCCT  
GGGGCCTGGGTGCAGGGCTGCCCATCCGGCTGCCAGTGCAAGCCAGCACAGACAGTCTTCT  
GCACTGCCGCCAGGGACCACGGTCCCCGAGACGTGCCACCCGACACGGTGGGCTGTAC  
GTCTTGAGAACGGCATCACCATGCTGACGCAAGCAGCTTGCCGGCCTGCCGGCCTGCA  
GCTCCTGGACCTGTACAGAACCGAGATGCCAGCCTGCCCTGCCCTGCCGGCATCCTGGACACTGCCAACGTGGAG  
ACCTCAGCCACAACAGCCTCCTGCCCTGGAGCCGGCATCCTGGACACTGCCAACGTGGAG  
GCGCTGCCGGCTGGCTGGTCTGGGCTGCAGCAGCTGGACGAGGGCTTCAAGCCGTTGCG  
CAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAG  
GCCTCCGGGGCCTGACGCCCTGCCGGCTGCCGGAACACCCGATTGCCAGCTGCCGGCCC  
GAGGACCTGCCGGCCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAACGCTGCCAGGC  
CCTGCCTGGCACCTCTGCCCTCTTCCCCGCCCTGCCCTGCGCTGCTGGCAGCTGCCGCAACC  
CCTCAACTGCGTGTGCCCTGAGCTGGTTGGCCCTGGGTGCGCGAGAGGCCACGTAC  
CTGCCAGCCCTGAGGAGACGCCCTGCCACTTCCGCCAACAGCCTGCCGGCTGCTCCT  
GGAGCTTGAACAGCCACTTGGCTGCCAGCCACCAACACCACAGCCACAGTCCACCA  
CGAGGCCGTGGTGGAGCCACAGCCTGTCTTAGCTTGGCTCCTACCTGGCTTAGC  
CCCACAGGCCGGCCACTGAGGCCAGGCCCTCCACTGCCAACCGACTGTAGGGCC  
TGTCCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCCTCAATGGGGCACATGCCACCTGG  
GGACACGGCACCACTGGCGTCTGTGCCCGAAGGCTTACGGGCTGTACTGTGAGAGC  
CAGATGGGGCAGGGACACGCCAGGCCACACCAGTCAGCCGAGGCCACACGGCC  
GACCCCTGGCATCGAGCCGTGAGGCCACCTCCCTGCCGTGGGCTGCAGCGTACCTCC  
AGGGGAGCTCCGTGAGCTCAGGAGCCTCCGTCTCACCTATCGAACCTATGGGCCCTGAT  
AAGCGGCTGGTGAACGCTGCCACTGCCCTCGCTGAGTACACGGTACCCAGCTGCG  
GCCAACGCCACTTAACCGTCTGTCTGCCTTGGGGCCGGGTGCCGGAGGGCG  
AGGAGGCCTGCCGGAGGCCATACACCCCAAGCCGTCCACTCCAACCACGCCAGTCACC  
CAGGCCCGCAGGGCAACCTGCCCTCCATTGCCCGCCCTGCCCGGGTGCCTGGC  
CGCGCTGGCTGCCGTGGGGCAGGCCACTGTGTGCCGGGGGGCCATGCCAGCAGCG  
CTCAGGACAAAGGGCAGGTGGGCCAGGGCTGGGCCCTGGAACCTGGAGGGAGTGAAGGTC  
CCCTGGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGCTGA  
GTGTGAGGTGCCACTCATGGCTTCCCAGGGCCTGCCCTCAGTCACCCCTCACGCAAAGC  
CCTACATTAAGCCCAGAGAGAGACAGGGCAGCTGGGCCGGCTCTCAGCCAGTGAGATGGC  
CAGCCCCCTCTGCCACACCACGTAAGTTCTCAGTCCCAACCTGCCGGATGTGCGAGA  
CAGGGCTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAG  
ATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCTATGAGGACAGTGT  
CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGCACGGCGGGCCCTGCCATGTGCTGGTAAC  
GCATGCCCTGGGCCCTGCTGGCTCTCCACTCCAGGCCACCTGGGGCCAGTGAAGGAAG  
CTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGACTCTAGTCTGGCCCGAGG  
AAGCGAAGGAACAAAAGAAACTGGAAAGGAAGATGCTTAGGAACATGTTGCTTTAA  
AATATATATATTTATAAGAGATCCTTCCCATTATTCTGGAAAGATGTTTCAAAC  
AGAGACAAGGACTTGGTTTGTAAGACAAACGATGATATGAAGGCCTTTGTAAGAAAAA  
ATAAAAAAAAAA

## **FIGURE 26**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804
<subunit 1 of 1, 598 aa, 1 stop
<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVPLLLPLLLLALGPGVQGCPGQCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYFEN
GIITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLDLSHNSLLALEPGILDNTANVEALRL
AGLGLQQQLDEGLFSRLRNLDLVDSDNQLERVPPVIRGLRGLTRRLLAGNTRIAQLRPEDLA
GLAALQELDVSNLSQLPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRESHVTLASP
EETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSLAPTWLSPTAP
ATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQ
GTRPSPTPVTPRPPRSLTGLIEPVSPPTSLRVGLQRYLQGSSVQLRSRLTYRNLSGPDKRLV
TLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEAACGEAHTPPAVHSNHAPVTQARE
GNLPLLIAPALAAVLLAALAAVGAAAYCVRGRAMAAAQDKQVGPGAGPLEGVKVPLEP
GPKATEGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI
```

**Signal sequence.**

amino acids 1-23

**Transmembrane domain.**

amino acids 501-522

**N-glycosylation sites.**

amino acids 198-202, 425-429, 453-457

**Tyrosine kinase phosphorylation site.**

amino acids 262-270

**N-myristoylation sites.**

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**EGF-like domain cysteine pattern signature.**

amino acids 355-367

**Leucine zipper pattern.**

amino acids 122-144, 194-216

## **FIGURE 27**

GGCACTAGGACAACCTTCTCCCTCTGCACCACTGCCGTACCCCTAACCGCCCCGCCACC  
TCCTTGCTACCCACTCTGAAACCACAGCTGTTGGCAGGGTCCCCAGCT**CATG**CCAGCCTC  
ATCTCCTTCTTGCTAGCCCCAAAGGGCCTCCAGGAACATGGGGGGCCCAGTCAGAGAGC  
CGGCACCTCTCAGTTGCCCTCTGGTGAGTTGGGGGCAGCTCTGGGGCCGTGGTTGTGCC  
ATGGCTCTGCTGACCAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA  
GGGGACAGGAGGCCCCCTCCAGAATGGGAAGGGTATCCCTGGCAGAGTCTCCGGAGCAGA  
GTTCCGATGCCCTGGAAGCCTGGAGAGATGGGAGAGATCCCGAAAAGGAGAGCAGTGCTC  
ACCCAAAAACAGAAGAAGCAGCACTCTGTCCTGCACCTGGTCCCATTACGCCACCTCAA  
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGCGTGGAGAGGCCTAC  
AGGCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTATCTGCTGTAGCCAGGTC  
CTGTTCAAGACGTGACTTCACCATGGTCAGGTGGTGTCTCGAGAAGGCCAAGGAAGGCA  
GGAGACTCTATTCGATGTATAAGAAGTATGCCCTCCCACCCGGACCAGGGCTACAACAGCT  
GCTATAGCGCAGGTGTCTCCATTACACCAAGGGATATTCTGAGTGTCTAATTCCCCGG  
GCAAGGGCGAAACTTAACCTCTCCACATGGAACCTCCTGGGTTGTGAAACTG**TGATT**  
GTGTTATAAAAGTGGCTCCAGCTTGGAGACCAGGGTGGGTACATACTGGAGACAGCCAA  
GAGCTGAGTATATAAGGAGAGGAATGTGCAGGAACAGAGGCATCTCCTGGGTTGGCTC  
CCCGTTCTCACTTCCCTTTCATTCCCACCCCTAGACTTGTGATTTACGGATATCTTG  
CTTCTGTTCCCCATGGAGCTCCG

## **FIGURE 28**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27433, pI: 9.85, NX(S/T): 2
MPASSPFL LAPKGPPGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTELQSLRREV
SRLQGTGGPSQN GEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTQKQKKQHSVLHLVPIN
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFMGQVVSREG
QGRQETLFRCIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARAKLNLSPHGTFLGFVKL
```

**Signal sequence.**

amino acids 1-40

**N-glycosylation site.**

amino acids 124-128

**Tyrosine kinase phosphorylation site.**

amino acids 156-164

**N-myristoylation site.**

amino acids 36-42, 40-46, 179-185, 242-248

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 34-45

## **FIGURE 29**

CACTTTCTCCCTCTCTTACTTCGAGAAACCGCGCTTCCGCTCTGGTCGCAGAGAC  
CTCGGAGACCGCGCCGGGAGACGGAGGTGCTGTGGTGGGGGGACCTGTGGCTGCTCGTA  
CCGCCCCCCCACCCCTCTGCACTGCCGTCTCCGGAAGAACCTTTCCCTGCTCTGTT  
TCCTTCACCGAGTCTGTGCATGCCCGGACCTGGCCGGAGGAGGCTGGCCGGCGGGAGA  
TGCTCTAGGGGCGGCGCGGGAGGAGCAGGCGGGACGGAGGGCCGGCAGGAAGATGGC  
TCCCCTGGACAGGGACTCTGCTGGCGTACTGCCGTCTGCCCTGCCTCTGGCTGGT  
CCTGAGTCGTGTGCCCATGTCCAGGGGAACAGCAGGAGTGGGAGGGACTGAGGAGCTGC  
CGTCGCCTCCGGACCATGCCGAGAGGGCTGAAGAACAAACATGAAAAAATACAGGCCAGTCAG  
GACCAGGGCTCCGTCTCCGGCTTGCGCTGCTGTGACCCGGTACCTCCATGTACCC  
GGCGACCGCCGTGCCCATCAACATCACTATCTGAAAGGGAGAAGGGTGAACGGAG  
ATCGAGGCCTCCAAGGGAAATATGGCAAACACAGGCTCAGCAGGGCCAGGGGCCACACTGGA  
CCCAAAGGGCAGAAGGGCTCATGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC  
CTTTTGGTGGGCCGGAAAGAACCCATGCACAGCAACCACACTACCAAGACGGTATCTCG  
ACACGGAGTCGTGAACCTCTACGACCACCTCAACATGTTACCGGAAGTTCTACTGCTAC  
GTGCCCGGCCTCTACTTCTCAGCCTCAACGTGCACACCTGGAACCAGAAGGAGACCTACCT  
GCACATCATGAAGAACGAGGAGGGTGGTATCTGTCGCGCAGGTGGGACCGCAGCA  
TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGTACGCC  
TACAAGGGCGAACGTGAGAACGCCATCTCAGCGAGGAGCTGGACACCTACATCAC  
TGGCTACCTGGTCAAGCACGCCACCGAGCCTAGCTGGCCGGCCACCTCCTCTCGCC  
ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTTCCCGATCCCTGGACTCCGACTC  
CCTGGCTTGGCATTCACTGAGACGCCCTGCACACACAGAAAGCCAAGCGATCGGTGCTCC  
CAGATCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAAGGGGGCACCCGC  
GAGAACCCCTCTGGGACCTCCGCAGGGCTCTCTGACACATCCTCAAGTGACCCGCACGGC  
GAGACGGGGTGGCGGCAGGGCTCCAGGGTGCAGGCGACCGCGGCTCCAGTCCTGGAAATA  
ATTAGGCAAATTCTAAAGGTCTAAAAGGAGCAAAGTAAACCGTAGGAACTTCTTGAGGGATAGGTGGACC  
TTGTTATTTTGTCTTCCAGCCAGCCTGCTGGCTCCAAGAGAGAGGGCTTTCAGTTGAG  
ACTCTGCTTAAGAGAAGATCAAAGTTAAAGCTCTGGGTCAAGGGAGGGGCCGGGAGG  
AAACTACCTCTGGCTTAATTCTTTAAGCACGTAGGAACCTTCTTGAGGGATAGGTGGACC  
CTGACATCCCTGTGGCCTTGCCAAAGGGCTCTGCTGGTCTTCTGAGTCACAGCTGCGAGGT  
GATGGGGCTGGGCCAGCGTCAGCCTCCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC  
TCCAGGGTGGTAGAAGCAGCCGAAGGGCTCTGACAGTGGCAGGGACCCCTGGTCCCCA  
GGCCTGCAGATGTTCTATGAGGGCAGAGCTCCTGGTACATCCATGTGTGGCTCTGCTCC  
ACCCCTGTGCCACCCAGAGCCTGGGGGTGGCTCCATGCCACCCCTGGCATCGGCT  
TTCTGTGCCGCCTCCCACACAAATCAGCCCCAGAAGGCCCCGGGCCCTGGCTCTGTTTT  
TATAAAACACCTCAAGCAGCACTGCAGTCTCCATCCTCGTGGCTAAGCATACCGCTT  
CCACGTGTGTTGGCAGCAAGGCTGATCCAGACCCCTCTGCCCTGCCCCACTGCCCT  
CATCCAGGCCTCTGACCAGTAGCCTGAGAGGGCTTTCTAGGCTTCAGAGCAGGGAGAG  
CTGGAAGGGCTAGAAAGCTCCGCTTGTCTGTTCTCAGGCTCCTGTGAGCCTCAGTCTG  
AGACCAGAGTCAAGAGGAAGTACACGTCCAATCACCGTGTAGGATTCACTCTCAGGAGC  
TGGGTGGCAGGAGAGGCAATAGCCCTGTGGCAATTGCAGGACCACTGGAGCAGGGTTGCG  
GTGTCTCCACGGTCTCTGCCCTGCCATGGCAGGGACTCTGATCTCCAGGAACCC  
ATAGCCCCCTCTCCACCTCACCCATGTTGATGCCAGGGTCACTCTGCTACCCGCTGGGCC  
CCCAAACCCCGCTGCCCTCTCCCTCCCCCATCCCCCACCTGGTTTGACTAATCCTGC  
TTCCCTCTCTGGGCTGGCTGCCGGATCTGGGTCCCTAAGTCCCTCTCTTAAAGAACTT  
CTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGCGTGCCCCGGAAGCAGAGGCCACACTC  
GCTGCTTAAGCTCCCCAGCTTTCCAGAAAATTAACACTCAGAATTGTGTTCAA

## **FIGURE 30**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MGSRGQGLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRP
SQDQGLPASRCLRCCDPGTSMYPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH
TGPKGQKGSMGAPGERCKSHYAAFSGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMF TGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAIFSEELDTYITFSGYLVKHATEP
```

**Signal sequence.**

amino acids 1-25

**N-glycosylation site.**

amino acids 93-97

**N-myristoylation sites.**

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

**Amidation site.**

amino acids 150-154

**Cell attachment sequence.**

amino acids 104-107

## **FIGURE 31**

CGGGAGCATCCGCTGCCTCGCCGAGACCCCCCGCGGGATTGCCCGGTCTTCCCGGG  
GCGCGACAGAGCTGCCTCGCACCTGGATGGCAGCAGGGCGCCGGGTCTCTGACGCCA  
GAGAGAAATCTCATCATCTGTGCAGCCTTAAAGCAAACATAAGACCAAGGGGAGGATTAT  
CCTTGACCTTGAAAGACCAAAACTAAACTGAAATTAAAATGTTCTCGGGGGAGAAGGGAG  
CTTGACTTACACTTGGTAATAATTGCTCCTGACACTAAGGCTGCTGCTAGTCAGAATT  
GCCTCAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTCTAAGGAATC  
AGAGGCAATGAGCCGTATATACTTCAACTCAAGAAGACTGCATTAATTCTGCTGTTCAAC  
AAAAAACATATCAGGGACAAAGCATGTAACTTGATGATCTCGACACTCGAAAAACAGCTA  
GACAACCCAACGTACCTATTTCTGTCCTAACGAGGAAGCCTGCAATTGAAACCAGCA  
AAAGGACTTATGAGTTACAGGATAATTACAGATTTCATCTTGCACAGAAATTGCCAAG  
CCAAGAGTTACCCCAGGAAGATTCTCTTACATGCCAATTTCACAAGCAGTCACCTCCC  
TAGCCCCATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT  
CAGAAGTTGGATCCTCAGATCACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTCCCCA  
GCTCCTGCTATAAGGAAAAGGCCATTCTCAGAGTCACAATTTCCTGATCAAGAAA  
TAGCTCATCTGCTGCCTGAAAATGTGAGTGCCTCCAGCTACGGTGGCAGTGCTCTCCA  
CATACCACCTCGGCTACTCCAAAGCCCACCCCTCTACCCACCAATGCTTCAGTGACACC  
TTCTGGGACTTCCCAGCCACAGCTGGCACCACAGCTCCACCTGTAACCACGTCACTCTC  
AGCCTCCCACGACCCTCATTTCTACAGTTTACACGGCTGCGGCTACACTCCAAGGAATG  
GCTACAAACAGCAGTTCTGACTACCACCTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA  
AACCATACCGTTACAGAAATCTCAAACCTTAACTTGAACACAGGAAATGTGTATAACCCTA  
CTGCACTTCTATGTCAAATGTGGAGTCTCCACTATGAATAAAACTGCTTCCTGGGAAGGT  
AGGGAGGCCAGTCCAGGCAGTTCCCTCCAGGGCAGTGTCCAGAAAATCAGTACGGCCTTCC  
ATTGAAAAATGGCTTCTTATCGGGTCCCTGCTTTGGTGTCTGTTGGTGTAGGCC  
TCGTCTCCTGGTAGAACCTTCAGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT  
TATTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACTCGGTGTCTCTTAATTCTATT  
TAGTAACCAGAACCCAAATGCAATGAGTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG  
TATTGAAAGACAGGAAATGCCCTCTGCTTTCTTGGAGACAGAGTCTT  
GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGAACCTCCGTCTC  
CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCTAAGTATCTGGGATTACAGGCATGTGCCA  
CCACACCTGGGTGATTTGTATTTAGAGACGGGTTCACCATGTTGGTCAGGCTG  
GTCTCAAACCTCGACCTAGTGATCCACCCCTCGGCCTCCAAAGTGTGGATTACAGG  
CATGAGCCACCACAGCTGGCCCCCTCTGTTTATGTTGGTTTGAGAAGGAATGAAGTG  
GGAACCAAATTAGGTAATTGGGTAATCTGTCTCTAAATATTAGCTAAAACAAAGCTCT  
ATGTAAGTAATAAGTATAATTGCCATATAAATTCAAACCTGGCTTTATGCAAA  
GAAACAGGTTAGGACATCTAGGTTCCAATTCAATTCTGGTTCCAGATAAAATCAAC  
TGTTTATATCAATTCTAATGGATTGCTTTCTTTATATGGATTCCCTTAAACTTATT  
CCAGATGTAGTCCTCCAATTAAATATTGAATAATCTTGTACTCAA

BIO 1650

## **FIGURE 32**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPPTLISTVFTRAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTAWEGRASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVDI
```

**Signal sequence.**

amino acids 1-25

**Transmembrane domain.**

amino acids 384-405

**N-glycosylation sites.**

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 415-419

**Tyrosine kinase phosphorylation site.**

amino acids 50-57

**N-myristoylation sites.**

amino acids 4-10, 48-54, 315-321

## **FIGURE 33**

GC GG CAC CTG G AAG **ATG** CGCC CATT GG CTGG TGG CCTG CTCA AGGTGGT GTTC GTGGT CTT C  
GC CCT CTT GTGT GCCT GGGT ATT CGGGG TACCT GCT CGCAG AGC TCA TT CCAG ATGC ACCC CT  
GTCC AGTG CTGC CTAT AGCATCC GCAG CATCGGGGAGAGGCCTG CTC TCAA AGCT CCAGT CC  
CCAAAAGGCAAAATGTGACC ACTGGACTCCCTGCCATCTGACACCTATGCCTACAGGTTA  
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAATCTGCTTGAGGATAACCTACTTATGGG  
AGAACAGCTGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAAC TGGA  
ATGTGACAGCAACACGATGTTTGATATGTATGAAGGCATACTCTGGACCGATGACA AAG  
TTTATTCA GAGTGCTGCTCCAAATCCCTGCTCTCATGGT GACCTATGACGACGGAAAGCAC  
AAGACTGAATAACGATGCCAAGAATGCCATAGAACGCACTTGGAAAGTAAAGAAATCAGGAACA  
TGAAATTCA GAGTCTAGCTGGTATT TATTGCAGCAAAAGGCTTGGAACTCCCTCCGAAATT  
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACACAGATATTCTGGCTGGCCTGCAGA  
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGC**TGA**ACTGCAGGGT CCTGAGTAAAT  
GTGTTCTGTATAAACAAATGCAGCTGGAAATCGCTCAAGAATCTTATT TTCTAAATCCAACA  
GCCCATATTGATGAGTATT TGGTTGTAAACCAATGAACATTGCTAGTTGTATCA  
AATCTTGGTACGCAGTATT TATACCA GTATT TATGTAGTGAAGATGTCAATTAGCAGGA  
AACTAAAATGAATGGAAATTCTTAAAAA AAAAAA

650  
649  
648  
647  
646  
645  
644  
643  
642  
641  
640

## **FIGURE 34**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777
><subunit 1 of 1, 235 aa, 1 stop
><MW: 25982, pI: 9.09, NX(S/T): 2
MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMDYEGDNGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS
```

**Signal sequence.**

amino acids 1-20

**N-glycosylation sites.**

amino acids 120-124, 208-212

**Glycosaminoglycan attachment site.**

amino acids 80-84

**N-myristoylation sites.**

amino acids 81-87, 108-114, 119-125